

OIPF

RAW SEQUENCE LISTING  
PATENT APPLICATION: US/09/528,031

DATE: 07/30/2001  
TIME: 15:59:55

Input Set : A:\seq1st.txt  
Output Set: N:\CRF3\07302001\I528031.raw

**ENTERED**

# SEQUENCE LISTING

4 (1) GENERAL INFORMATION:  
6 (i) APPLICANT: SHYJAN, Andrew  
8 (ii) TITLE OF INVENTION: NOVEL MULTIDRUG RESISTANCE-ASSOCIATED  
9 POLYPEPTIDE  
11 (iii) NUMBER OF SEQUENCES: 8  
13 (iv) CORRESPONDENCE ADDRESS:  
14 (A) ADDRESSEE: LAHIVE & COCKFIELD, LLP  
15 (B) STREET: 28 State Street  
16 (C) CITY: Boston  
17 (D) STATE: Massachusetts  
18 (E) COUNTRY: USA  
19 (F) ZIP: 02109  
21 (v) COMPUTER READABLE FORM:  
22 (A) MEDIUM TYPE: Floppy disk  
23 (B) COMPUTER: IBM PC compatible  
24 (C) OPERATING SYSTEM: PC-DOS/MS-DOS  
25 (D) SOFTWARE: PatentIn Release #1.0, Version #1.30  
27 (vi) CURRENT APPLICATION DATA:  
C--> 28 (A) APPLICATION NUMBER: US/09/528,031  
C--> 29 (B) FILING DATE: 17-Mar-2001  
30 (C) CLASSIFICATION:  
32 (viii) ATTORNEY/AGENT INFORMATION:  
33 (A) NAME: Elizabeth A. Hanley  
34 (B) REGISTRATION NUMBER: 33,505  
35 (C) REFERENCE/DOCKET NUMBER: MNI-056CP  
37 (ix) TELECOMMUNICATION INFORMATION:  
38 (A) TELEPHONE: (617) 227-7400  
39 (B) TELEFAX: (617) 742-4214  
42 (2) INFORMATION FOR SEQ ID NO: 1:  
44 (i) SEQUENCE CHARACTERISTICS:  
45 (A) LENGTH: 4847 base pairs  
46 (B) TYPE: nucleic acid  
47 (C) STRANDEDNESS: single  
48 (D) TOPOLOGY: linear  
50 (ix) FEATURE:  
51 (A) NAME/KEY: CDS  
52 (B) LOCATION: 116..4426  
54 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:  
56 GGCTCATGCT CGGGAGCGTG GTTGAGCGGC TGGCGCGGTT GTCCTGGAGC AGGGGCGCAG 60  
58 GAATTCTGAT GTGAACTAA CAGTCTGTGA GCCCTGGAAC CTCCACTCAG AGAAG ATG 118  
59 Met  
60 1  
62 AAG GAT ATC GAC ATA GGA AAA GAG TAT ATC ATC CCC AGT CCT GGG TAT 166  
63 Lys Asp Ile Asp Ile Gly Lys Glu Tyr Ile Ile Pro Ser Pro Gly Tyr  
64 5 10 15  
66 AGA AGT GTG AGG GAG AGA ACC AGC ACT TCT GGG ACG CAC AGA GAC CGT 214

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67	Arg	Ser	Val	Arg	Glu	Arg	Thr	Ser	Thr	Ser	Gly	Thr	His	Arg	Asp	Arg	
68			20					25					30				
70	GAA	GAT	TCC	AAG	TTC	AGG	AGA	ACT	CGA	CCG	TTG	GAA	TGC	CAA	GAT	GCC	262
71	Glu	Asp	Ser	Lys	Phe	Arg	Arg	Thr	Arg	Pro	Leu	Glu	Cys	Gln	Asp	Ala	
72			35					40				45					
74	TTG	GAA	ACA	GCA	GCC	CGA	GCC	GAG	GGC	CTC	TCT	CTT	GAT	GCC	TCC	ATG	310
75	Leu	Glu	Thr	Ala	Ala	Arg	Ala	Glu	Gly	Leu	Ser	Leu	Asp	Ala	Ser	Met	
76	50					55				60						65	
78	CAT	TCT	CAG	CTC	AGA	ATC	CTG	GAT	GAG	GAG	CAT	CCC	AAG	GGA	AAG	TAC	358
79	His	Ser	Gln	Leu	Arg	Ile	Leu	Asp	Glu	Glu	His	Pro	Lys	Gly	Lys	Tyr	
80					70					75					80		
82	CAT	CAT	GGC	TTG	AGT	GCT	CTG	AAG	CCC	ATC	CGG	ACT	ACT	TGC	AAA	CAC	406
83	His	His	Gly	Leu	Ser	Ala	Leu	Lys	Pro	Ile	Arg	Thr	Thr	Cys	Lys	His	
84			85						90					95			
86	CAG	CAC	CCA	GTG	GAC	AAT	GCT	GGG	CTT	TTT	TCC	TGT	ATG	ACT	TTT	TCG	454
87	Gln	His	Pro	Val	Asp	Asn	Ala	Gly	Leu	Phe	Ser	Cys	Met	Thr	Phe	Ser	
88			100					105					110				
90	TGG	CTT	TCT	TCT	CTG	GCC	CGT	GTG	GCC	CAC	AAG	AAG	GGG	GAG	CTC	TCA	502
91	Trp	Leu	Ser	Ser	Leu	Ala	Arg	Val	Ala	His	Lys	Lys	Gly	Glu	Leu	Ser	
92		115					120					125					
94	ATG	GAA	GAC	GTG	TGG	TCT	CTG	TCC	AAG	CAC	GAG	TCT	TCT	GAC	GTG	AAC	550
95	Met	Glu	Asp	Val	Trp	Ser	Leu	Ser	Lys	His	Glu	Ser	Ser	Asp	Val	Asn	
96	130					135				140					145		
98	TGC	AGA	AGA	CTA	GAG	AGA	CTG	TGG	CAA	GAA	GAG	CTG	AAT	GAA	GTT	GGG	598
99	Cys	Arg	Arg	Leu	Glu	Arg	Leu	Trp	Gln	Glu	Glu	Leu	Asn	Glu	Val	Gly	
100				150					155				160				
102	CCA	GAC	GCT	GCT	TCC	CTG	CGA	AGG	GTT	GTG	TGG	ATC	TTC	TGC	CGC	ACC	646
103	Pro	Asp	Ala	Ala	Ser	Leu	Arg	Arg	Val	Val	Trp	Ile	Phe	Cys	Arg	Thr	
104			165					170					175				
106	AGG	CTC	ATC	CTG	TCC	ATC	GTG	TGC	CTG	ATG	ATC	ACG	CAG	CTG	GCT	GGC	694
107	Arg	Leu	Ile	Leu	Ser	Ile	Val	Cys	Leu	Met	Ile	Thr	Gln	Leu	Ala	Gly	
108			180					185					190				
110	TTC	AGT	GGA	CCA	GCC	TTC	ATG	GTG	AAA	CAC	CTC	TTG	GAG	TAT	ACC	CAG	742
111	Phe	Ser	Gly	Pro	Ala	Phe	Met	Val	Lys	His	Leu	Leu	Glu	Tyr	Thr	Gln	
112		195				200					205						
114	GCA	ACA	GAG	TCT	AAC	CTG	CAG	TAC	AGC	TTG	TTG	TTA	GTG	CTG	GGC	CTC	790
115	Ala	Thr	Glu	Ser	Asn	Leu	Gln	Tyr	Ser	Leu	Leu	Leu	Val	Leu	Gly	Leu	
116	210				215					220					225		
118	CTC	CTG	ACG	GAA	ATC	GTG	CGG	TCT	TGG	TCG	CTT	GCA	CTG	ACT	TGG	GCA	838
119	Leu	Leu	Thr	Glu	Ile	Val	Arg	Ser	Trp	Ser	Leu	Ala	Leu	Thr	Trp	Ala	
120				230					235				240				
122	TTG	AAT	TAC	CGA	ACC	GGT	GTC	CGC	TTG	CGG	GGG	GCC	ATC	CTA	ACC	ATG	886
123	Leu	Asn	Tyr	Arg	Thr	Gly	Val	Arg	Leu	Arg	Gly	Ala	Ile	Leu	Thr	Met	
124			245					250					255				
126	GCA	TTT	AAG	AAG	ATC	CTT	AAG	TTA	AAG	AAC	ATT	AAA	GAG	AAA	TCC	CTG	934
127	Ala	Phe	Lys	Lys	Ile	Leu	Lys	Leu	Lys	Asn	Ile	Lys	Glu	Lys	Ser	Leu	
128		260				265					270						
130	GGT	GAG	CTC	ATC	AAC	ATT	TGC	TCC	AAC	GAT	GGG	CAG	AGA	ATG	TTT	GAG	982
131	Gly	Glu	Leu	Ile	Asn	Ile	Cys	Ser	Asn	Asp	Gly	Gln	Arg	Met	Phe	Glu	

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132	275	280	285	
134	GCA GCA GCC GTT GGC AGC CTG CTG GCT GGA GGA CCC GTT GTT GCC ATC			1030
135	Ala Ala Ala Val Gly Ser Leu Leu Ala Gly Gly Pro Val Val Ala Ile			
136	290	295	300	305
138	TTA GGC ATG ATT TAT AAT GTA ATT ATT CTG GGA CCA ACA GGC TTC CTG			1078
139	Leu Gly Met Ile Tyr Asn Val Ile Ile Leu Gly Pro Thr Gly Phe Leu			
140		310	315	320
142	GGA TCA GCT GTT TTT ATC CTC TTT TAC CCA GCA ATG ATG TTT GCA TCA			1126
143	Gly Ser Ala Val Phe Ile Leu Phe Tyr Pro Ala Met Met Phe Ala Ser			
144		325	330	335
146	CGG CTC ACA GCA TAT TTC AGG AGA AAA TGC GTG GCC GCC ACG GAT GAA			1174
147	Arg Leu Thr Ala Tyr Phe Arg Arg Lys Cys Val Ala Ala Thr Asp Glu			
148		340	345	350
150	CGT GTC CAG AAG ATG AAT GAA GTT CTT ACT TAC ATT AAA TTT ATC AAA			1222
151	Arg Val Gln Lys Met Asn Glu Val Leu Thr Tyr Ile Lys Phe Ile Lys			
152		355	360	365
154	ATG TAT GCC TGG GTC AAA GCA TTT TCT CAG AGT GTT CAG AAA ATC CGC			1270
155	Met Tyr Ala Trp Val Lys Ala Phe Ser Gln Ser Val Gln Lys Ile Arg			
156	370	375	380	385
158	GAG GAG GAG CGT CGG ATA TTG GAA AAA GCC GGG TAC TTC CAG AGC ATC			1318
159	Glu Glu Glu Arg Arg Ile Leu Glu Lys Ala Gly Tyr Phe Gln Ser Ile			
160		390	395	400
162	ACT GTG GGT GTG GCT CCC ATT GTG GTG GTG ATT GCC AGC GTG GTG ACC			1366
163	Thr Val Gly Val Ala Pro Ile Val Val Val Ile Ala Ser Val Val Thr			
164		405	410	415
166	TTC TCT GTT CAT ATG ACC CTG GGC TTC GAT CTG ACA GCA GCA CAG GCT			1414
167	Phe Ser Val His Met Thr Leu Gly Phe Asp Leu Thr Ala Ala Gln Ala			
168		420	425	430
170	TTC ACA GTG GTG ACA GTC TTC AAT TCC ATG ACT TTT GCT TTG AAA GTA			1462
171	Phe Thr Val Val Thr Val Phe Asn Ser Met Thr Phe Ala Leu Lys Val			
172		435	440	445
174	ACA CCG TTT TCA GTA AAG TCC CTC TCA GAA GCC TCA GTG GCT GTT GAC			1510
175	Thr Pro Phe Ser Val Lys Ser Leu Ser Glu Ala Ser Val Ala Val Asp			
176	450	455	460	465
178	AGA TTT AAG AGT TTG TTT CTA ATG GAA GAG GTT CAC ATG ATA AAG AAC			1558
179	Arg Phe Lys Ser Leu Phe Leu Met Glu Glu Val His Met Ile Lys Asn			
180		470	475	480
182	AAA CCA GCC AGT CCT CAC ATC AAG ATA GAG ATG AAA AAT GCC ACC TTG			1606
183	Lys Pro Ala Ser Pro His Ile Lys Ile Glu Met Lys Asn Ala Thr Leu			
184		485	490	495
186	GCA TGG GAC TCC TCC CAC TCC AGT ATC CAG AAC TCG CCC AAG CTG ACC			1654
187	Ala Trp Asp Ser Ser His Ser Ser Ile Gln Asn Ser Pro Lys Leu Thr			
188		500	505	510
190	CCC AAA ATG AAA AAA GAC AAG AGG GCT TCC AGG GGC AAG AAA GAG AAG			1702
191	Pro Lys Met Lys Lys Asp Lys Arg Ala Ser Arg Gly Lys Lys Glu Lys			
192		515	520	525
194	GTG AGG CAG CTG CAG CGC ACT GAG CAT CAG GCG GTG CTG GCA GAG CAG			1750
195	Val Arg Gln Leu Gln Arg Thr Glu His Gln Ala Val Leu Ala Glu Gln			
196	530	535	540	545

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198	AAA	GGC	CAC	CTC	CTC	CTG	GAC	AGT	GAC	GAG	CGG	CCC	AGT	CCC	GAA	GAG	1798
199	Lys	Gly	His	Leu	Leu	Leu	Asp	Ser	Asp	Glu	Arg	Pro	Ser	Pro	Glu	Glu	
200					550					555					560		
202	GAA	GAA	GGC	AAG	CAC	ATC	CAC	CTG	GGC	CAC	CTG	CGC	TTA	CAG	AGG	ACA	1846
203	Glu	Glu	Gly	Lys	His	Ile	His	Leu	Gly	His	Leu	Arg	Leu	Gln	Arg	Thr	
204				565					570					575			
206	CTG	CAC	AGC	ATC	GAT	CTG	GAG	ATC	CAA	GAG	GGT	AAA	CTG	GTT	GGA	ATC	1894
207	Leu	His	Ser	Ile	Asp	Leu	Glu	Ile	Gln	Glu	Gly	Lys	Leu	Val	Gly	Ile	
208			580					585					590				
210	TGC	GGC	AGT	GTG	GGA	AGT	GGA	AAA	ACC	TCT	CTC	ATT	TCA	GCC	ATT	TTA	1942
211	Cys	Gly	Ser	Val	Gly	Ser	Gly	Lys	Thr	Ser	Leu	Ile	Ser	Ala	Ile	Leu	
212		595				600						605					
214	GGC	CAG	ATG	ACG	CTT	CTA	GAG	GGC	AGC	ATT	GCA	ATC	AGT	GGA	ACC	TTC	1990
215	Gly	Gln	Met	Thr	Leu	Leu	Glu	Gly	Ser	Ile	Ala	Ile	Ser	Gly	Thr	Phe	
216	610					615					620					625	
218	GCT	TAT	GTG	GCC	CAG	CAG	GCC	TGG	ATC	CTC	AAT	GCT	ACT	CTG	AGA	GAC	2038
219	Ala	Tyr	Val	Ala	Gln	Gln	Ala	Trp	Ile	Leu	Asn	Ala	Thr	Leu	Arg	Asp	
220				630						635					640		
222	AAC	ATC	CTG	TTT	GGG	AAG	GAA	TAT	GAT	GAA	GAA	AGA	TAC	AAC	TCT	GTG	2086
223	Asn	Ile	Leu	Phe	Gly	Lys	Glu	Tyr	Asp	Glu	Glu	Arg	Tyr	Asn	Ser	Val	
224			645					650					655				
226	CTG	AAC	AGC	TGC	TGC	CTG	AGG	CCT	GAC	CTG	GCC	ATT	CTT	CCC	AGC	AGC	2134
227	Leu	Asn	Ser	Cys	Cys	Leu	Arg	Pro	Asp	Leu	Ala	Ile	Leu	Pro	Ser	Ser	
228			660					665					670				
230	GAC	CTG	ACG	GAG	ATT	GGA	GAG	CGA	GGA	GCC	AAC	CTG	AGC	GGT	GGG	CAG	2182
231	Asp	Leu	Thr	Glu	Ile	Gly	Glu	Arg	Gly	Ala	Asn	Leu	Ser	Gly	Gly	Gln	
232		675				680						685					
234	CGC	CAG	AGG	ATC	AGC	CTT	GCC	CGG	GCC	TTG	TAT	AGT	GAC	AGG	AGC	ATC	2230
235	Arg	Gln	Arg	Ile	Ser	Leu	Ala	Arg	Ala	Leu	Tyr	Ser	Asp	Arg	Ser	Ile	
236	690					695				700						705	
238	TAC	ATC	CTG	GAC	GAC	CCC	CTC	AGT	GCC	TTA	GAT	GCC	CAT	GTG	GGC	AAC	2278
239	Tyr	Ile	Leu	Asp	Asp	Pro	Leu	Ser	Ala	Leu	Asp	Ala	His	Val	Gly	Asn	
240				710						715					720		
242	CAC	ATC	TTC	AAT	AGT	GCT	ATC	CGG	AAA	CAT	CTC	AAG	TCC	AAG	ACA	GTT	2326
243	His	Ile	Phe	Asn	Ser	Ala	Ile	Arg	Lys	His	Leu	Lys	Ser	Lys	Thr	Val	
244			725					730					735				
246	CTG	TTT	GTT	ACC	CAC	CAG	TTA	CAG	TAC	CTG	GTT	GAC	TGT	GAT	GAA	GTG	2374
247	Leu	Phe	Val	Thr	His	Gln	Leu	Gln	Tyr	Leu	Val	Asp	Cys	Asp	Glu	Val	
248			740					745					750				
250	ATC	TTC	ATG	AAA	GAG	GGC	TGT	ATT	ACG	GAA	AGA	GGC	ACC	CAT	GAG	GAA	2422
251	Ile	Phe	Met	Lys	Glu	Gly	Cys	Ile	Thr	Glu	Arg	Gly	Thr	His	Glu	Glu	
252		755				760						765					
254	CTG	ATG	AAT	TTA	AAT	GGT	GAC	TAT	GCT	ACC	ATT	TTT	AAT	AAC	CTG	TTG	2470
255	Leu	Met	Asn	Leu	Asn	Gly	Asp	Tyr	Ala	Thr	Ile	Phe	Asn	Asn	Leu	Leu	
256	770					775					780					785	
258	CTG	GGA	GAG	ACA	CCG	CCA	GTT	GAG	ATC	AAT	TCA	AAA	AAG	GAA	ACC	AGT	2518
259	Leu	Gly	Glu	Thr	Pro	Pro	Val	Glu	Ile	Asn	Ser	Lys	Lys	Glu	Thr	Ser	
260				790						795					800		
262	GGT	TCA	CAG	AAG	AAG	TCA	CAA	GAC	AAG	GGT	CCT	AAA	ACA	GGA	TCA	ATA	2566

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263	Gly	Ser	Gln	Lys	Lys	Ser	Gln	Asp	Lys	Gly	Pro	Lys	Thr	Gly	Ser	Ile	
264				805					810					815			
266	AAG	AAG	GAA	AAA	GCA	GTA	AAG	CCA	GAG	GAA	GGG	CAG	CTT	GTG	CAG	CTG	2614
267	Lys	Lys	Glu	Lys	Ala	Val	Lys	Pro	Glu	Glu	Gly	Gln	Leu	Val	Gln	Leu	
268			820					825					830				
270	GAA	GAG	AAA	GGG	CAG	GGT	TCA	GTG	CCC	TGG	TCA	GTA	TAT	GGT	GTC	TAC	2662
271	Glu	Glu	Lys	Gly	Gln	Gly	Ser	Val	Pro	Trp	Ser	Val	Tyr	Gly	Val	Tyr	
272			835					840					845				
274	ATC	CAG	GCT	GCT	GGG	GGC	CCC	TTG	GCA	TTC	CTG	GTT	ATT	ATG	GCC	CTT	2710
275	Ile	Gln	Ala	Ala	Gly	Gly	Pro	Leu	Ala	Phe	Leu	Val	Ile	Met	Ala	Leu	
276	850					855					860					865	
278	TTC	ATG	CTG	AAT	GTA	GGC	AGC	ACC	GCC	TTC	AGC	ACC	TGG	TGG	TTG	AGT	2758
279	Phe	Met	Leu	Asn	Val	Gly	Ser	Thr	Ala	Phe	Ser	Thr	Trp	Trp	Leu	Ser	
280				870							875					880	
282	TAC	TGG	ATC	AAG	CAA	GGA	AGC	GGG	AAC	ACC	ACT	GTG	ACT	CGA	GGG	AAC	2806
283	Tyr	Trp	Ile	Lys	Gln	Gly	Ser	Gly	Asn	Thr	Thr	Val	Thr	Arg	Gly	Asn	
284				885					890					895			
286	GAG	ACC	TCG	GTG	AGT	GAC	AGC	ATG	AAG	GAC	AAT	CCT	CAT	ATG	CAG	TAC	2854
287	Glu	Thr	Ser	Val	Ser	Asp	Ser	Met	Lys	Asp	Asn	Pro	His	Met	Gln	Tyr	
288			900					905					910				
290	TAT	GCC	AGC	ATC	TAC	GCC	CTC	TCC	ATG	GCA	GTC	ATG	CTG	ATC	CTG	AAA	2902
291	Tyr	Ala	Ser	Ile	Tyr	Ala	Leu	Ser	Met	Ala	Val	Met	Leu	Ile	Leu	Lys	
292			915				920						925				
294	GCC	ATT	CGA	GGA	GTT	GTC	TTT	GTC	AAG	GGC	ACG	CTG	CGA	GCT	TCC	TCC	2950
295	Ala	Ile	Arg	Gly	Val	Val	Phe	Val	Lys	Gly	Thr	Leu	Arg	Ala	Ser	Ser	
296	930					935					940					945	
298	CGG	CTG	CAT	GAC	GAG	CTT	TTC	CGA	AGG	ATC	CTT	CGA	AGC	CCT	ATG	AAG	2998
299	Arg	Leu	His	Asp	Glu	Leu	Phe	Arg	Arg	Ile	Leu	Arg	Ser	Pro	Met	Lys	
300				950					955					960			
302	TTT	TTT	GAC	ACG	ACC	CCC	ACA	GGG	AGG	ATT	CTC	AAC	AGG	TTT	TCC	AAA	3046
303	Phe	Phe	Asp	Thr	Thr	Pro	Thr	Gly	Arg	Ile	Leu	Asn	Arg	Phe	Ser	Lys	
304				965					970					975			
306	GAC	ATG	GAT	GAA	GTT	GAC	GTG	CGG	CTG	CCG	TTC	CAG	GCC	GAG	ATG	TTC	3094
307	Asp	Met	Asp	Glu	Val	Asp	Val	Arg	Leu	Pro	Phe	Gln	Ala	Glu	Met	Phe	
308			980					985					990				
310	ATC	CAG	AAC	GTT	ATC	CTG	GTG	TTC	TTC	TGT	GTG	GGA	ATG	ATC	GCA	GGA	3142
311	Ile	Gln	Asn	Val	Ile	Leu	Val	Phe	Phe	Cys	Val	Gly	Met	Ile	Ala	Gly	
312			995				1000					1005					
314	GTC	TTC	CCG	TGG	TTC	CTT	GTG	GCA	GTG	GGG	CCC	CTT	GTC	ATC	CTC	TTT	3190
315	Val	Phe	Pro	Trp	Phe	Leu	Val	Ala	Val	Gly	Pro	Leu	Val	Ile	Leu	Phe	
316	1010					1015					1020					1025	
318	TCA	GTC	CTG	CAC	ATT	GTC	TCC	AGG	GTC	CTG	ATT	CGG	GAG	CTG	AAG	CGT	3238
319	Ser	Val	Leu	His	Ile	Val	Ser	Arg	Val	Leu	Ile	Arg	Glu	Leu	Lys	Arg	
320				1030						1035				1040			
322	CTG	GAC	AAT	ATC	ACG	CAG	TCA	CCT	TTC	CTC	TCC	CAC	ATC	ACG	TCC	AGC	3286
323	Leu	Asp	Asn	Ile	Thr	Gln	Ser	Pro	Phe	Leu	Ser	His	Ile	Thr	Ser	Ser	
324				1045					1050					1055			
326	ATA	CAG	GGC	CTT	GCC	ACC	ATC	CAC	GCC	TAC	AAT	AAA	GGG	CAG	GAG	TTT	3334
327	Ile	Gln	Gly	Leu	Ala	Thr	Ile	His	Ala	Tyr	Asn	Lys	Gly	Gln	Glu	Phe	

VERIFICATION SUMMARY

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L:28 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]

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